



(1)GENERAL INFORMATION:

(i)APPLICANT: KAWASAKI, Hideki
TOKAI, Masaya
KIKUCHI, Yasuhiro
OUCHI, Kozo

(ii)TITLE OF INVENTION:DNA ENCODING PROTEIN COMPLEMENTING
YEAST
LOW TEMPERATURE-SENSITIVE FERMENTABILITY

(iii)NUMBER OF SEQUENCES: 2

(iv)CORRESPONDENCE ADDRESS:

(A)ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
(B)STREET: 30 Rockefeller Plaza
(C)CITY: New York
(D)STATE: New York
(E)COUNTRY: U.S.A.
(F)ZIP: 10112-3801

(v)COMPUTER READABLE FORM:

(A)MEDIUM TYPE: Diskette - 3.50 inch, 1440 kb storage.

(B)COMPUTER: IBM PS/V
(C)OPERATING SYSTEM: MS-DOS Ver3.30
(D)SOFTWARE: PATENT AID Ver1.0

(vi)CURRENT APPLICATION DATA:

(A)APPLICATION NUMBER: 09/678,023
(B)FILING DATE: 04-OCTOBER-2000

(vii)PRIOR APPLICATION DATA:

(A)APPLICATION NUMBER: 08/894,344
(B)FILING DATE: 15-AUGUST-1997

(vii)PRIOR APPLICATION DATA:

(A)APPLICATION NUMBER: JP343700/95
(B)FILING DATE: 28-DECEMBER-1995
(A)APPLICATION NUMBER: PCT/JP96/03862
(B)FILING DATE: 27-DECEMBER-1996

(viii)ATTORNEY/AGENT INFORMATION:

(A)NAME: Perry, Lawrence S.
(B)REGISTRATION NUMBER: 31865

(ix)TELECOMMUNICATION INFORMATION:

(A)TELEPHONE: 212-218-2100
(B)TELEFAX: 212-218-2200

(2)INFORMATION FOR SEQ ID NO: 1 :

(i)SEQUENCE CHARACTERISTICS:

(A)LENGTH: 8874 base pairs
(B)TYPE: nucleic acid
(C)STRANDEDNESS: double
(D)TOPOLOGY: linear

(ii)MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: X2180-1B

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1 to 8874
 (C) IDENTIFICATION METHOD: E

(ix) FEATURE:
 (A) NAME/KEY: cleavage-site
 (B) LOCATION: 1291 to 1296
 (C) IDENTIFICATION METHOD: S

(ix) FEATURE:
 (A) NAME/KEY: cleavage-site
 (B) LOCATION: 4388 to 4393
 (C) IDENTIFICATION METHOD: S

(ix) FEATURE:
 (A) NAME/KEY: cleavage-site
 (B) LOCATION: 5027 to 5032
 (C) IDENTIFICATION METHOD: S

(ix) FEATURE:
 (A) NAME/KEY: cleavage-site
 (B) LOCATION: 7675 to 7680
 (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

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TGT TTG ACA ATG ATA TTC TAC ATG GGA AGA ATC TAT GCA TAC CTT GTA  144
AGT TTT ATA TTA GAA TGG CTA CTA TGG AAA CGA GCG AAA ATC AAG ATA  192
AAT GTT GAG ACA CTT CGT GTC TCC TTA CTA GGT GGT CGA ATA CAT TTT  240
AAA AAC CTT TCC GTA ATA CAC AAA GAT TAT ACA ATT TCG GTA TTA GAG  288
GGT AGT TTA ACA TGG AAA TAC TGG CTT TTA AAT TGC AGA AAA GCA GAA  336
TTG ATA GAG AAT AAC AAG TCT TCT TCT GGC AAA AAA GCA AAG CTT CCC  384
TGT AAA ATT TCC GTA GAA TGT GAA GGT CTA GAA ATT TTT ATT TAC AAC  432
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CGC GAT AAA TTT GAA AAA TAC CTT AAT GAG CAT TCT TTT CCT GAA CCT  528
TTT AGC GAT GGA AGT AGT GCT GAT AAA TTA GAT GAA GAT CTA AGC GAA  576
TCT GCA TAC ACA ACG AAC TCT GAT GCA TCA ATT GTT AAT GAC AGG GAC  624
TAC CAA GAA ACA GAT ATC GGC AAA CAT CCA AAG CTA CTG ATG TTT TTA  672
CCA ATT GAG CTT AAA TTT AGC CGC GGT TCC CTA CTG TTA GGA AAC AAA  720
TTC ACG CCA TCT GTT ATG ATT CTA AGT TAT GAA AGT GGA AAA GGC ATA  768
ATA GAT GTT TTA CCT CCA AAA GAG CGA TTA GAT TTA TAC AGA AAT AAA  816
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ACA CAG ATG GAA TTC AAA AAC TTC GAA ATT TCT ATC AAA CAA AAT ATT 864
 GGT TAC GAT GAT GCT ATT GGA TTG AAG TTT AAA ATA GAT AGA GGG AAA 912
 GTG TCA AAG TTA TGG AAA ACG TTT GTA CGA GTC TTT CAG ATA GTA ACC 960
 AAG CCT GTT GTA CCG AAA AAG ACT AAA AAA AGC GCA GGC ACA TCA GAT 1008
 GAC AAT TTC TAT CAT AAA TGG AAA GGT TTA TCT CTT TAT AAG GCT TCT 1056
 GCG GGC GAC GCT AAA GCA AGT GAT TTA GAT GAT GTT GAG TTC GAT TTG 1104
 ACG AAC CAT GAA TAT GCT AAA TTT ACA TCA ATT TTA AAA TGC CCA AAG 1152
 GTC ACA ATT GCA TAT GAC GTG GAT GTT CCG GGC GTT GTG CCA CAT GGT 1200
 GCA CAT CCG ACA ATA CCT GAT ATT GAT GGA CCA GAT GTG GGC AAT AAC 1248
 GGA GCA CCT CCA GAT TTT GCT TTA GAT GTT CAA ATT CAC GGA GGA TCC 1296
 ATC TGT TAC GGA CCT TGG GCT CAA AGA CAA GTC AGT CAT CTA CAA AGA 1344
 GTT CTA TCA CCG GTA GTT TCA AGG ACA GCC AAA CCT ATA AAA AAA CTC 1392
 CCG CCA GGT TCT AGA AGA ATA TAT ACA CTT TTC AGG ATG AAT ATA TCA 1440
 ATA ATG GAA GAT ACT ACT TGG CGT ATA CCG ACG AGG GAA AGT AGC AAA 1488
 GAC CCC GAA TTT TTG AAA CAC TAC AAA GAA ACT AAT GAA GAA TAT AGG 1536
 CCA TTT GGA TGG ATG GAT CTC CGA TTT TGT AAG GAC ACC TAT GCA AAT 1584
 TTC AAT ATA AGT GTT TGT CCT ACA GTG CAA GGT TTT CAG AAT AAT TTC 1632
 CAT GTT CAT TTC CTG GAA ACC GAA ATT AGG TCA AGT GTT AAT CAC GAT 1680
 ATT TTG TTA AAA AGC AAG GTA TTC GAT ATT GAT GGG GAT ATT GGA TAT 1728
 CCA TTG GGT TGG AAT AGC AAA GCT ATA TGG ATA ATT AAC ATG AAG TCA 1776
 GAA CAA TTA GAG GCG TTT CTG CTA CGT GAG CAT ATA ACT TTA GTT GCA 1824
 GAT ACG CTT TCA GAC TTT TCC GCT GGT GAT CCT ACG CCT TAC GAA CTT 1872
 TTT AGA CCA TTC GTA TAC AAA GTC AAT TGG GAA ATG GAA GGA TAT TCC 1920
 ATT TAC TTA AAC GTC AAT GAT CAC AAT ATT GTT AAC AAT CCG TTA GAT 1968
 TTT AAC GAA AAC TGT TAT TTA TCC CTT CAT GGT GAT AAG CTT TCA ATT 2016
 GAT GTC ACG GTA CCC CGT GAG AGT ATT TTG GGG ACA TAC ACA GAT ATG 2064
 TCC TAC GAG ATC TCA ACT CCA ATG TTC AGA ATG ATG TTA AAT ACC CCC 2112
 CCT TGG AAT ACA TTG AAC GAA TTC ATG AAA CAT AAA GAA GTG GGG AGA 2160
 GCA TAC GAC TTT ACA ATT AAA GGT TCT TAC CTT CTC TAT TCC GAG TTA 2208
 GAT ATT GAT AAT GTC GAT ACG CTA GTC ATA GAG TGT AAC AGC AAG AGT 2256
 ACA GTA CTT CAC TGC TAT GGG TTT GTC ATG AGG TAT TTA ACA AAC GTA 2304
 AAG ATG AAT TAC TTC GGT GAA TTT TTT AAT TTT GTG ACG TCA GAA GAG 2352

TAC ACA GGT GTC CTT GGC GCT AGG GAA GTC GGA GAT GTC ACT ACG AAA 2400
AGC TCG GTG GCA GAT TTG GCA TCT ACT GTA GAT TCA GGG TAC CAA AAT 2448
AGC AGT CTA AAG AAC GAA TCT GAG GAT AAA GGT CCT ATG AAA AGG TCA 2496
GAT TTG AAA AGG ACT ACC AAC GAA ACT GAT ATT TGG TTC ACA TTT TCG 2544
GTT TGG GAT GGT GCT CTG ATA TTA CCA GAA ACG ATT TAC AGT TTT GAT 2592
CCA TGC ATT GCA CTA CAT TTT GCC GAA CTT GTA GTG GAT TTC AGA AGT 2640
TGT AAT TAT TAT ATG GAC ATA ATG GCG GTT CTC AAC GGG ACT TCA ATA 2688
AAG CGG CAC GTT TCA AAA CAA ATA AAT GAA GTA TTT GAT TTT ATA CGT 2736
CGT AAT AAC GGA GCT GAT GAG CAA GAG CAC GGA TTG CTT TCG GAC CTC 2784
ACC ATT CAT GGA CAT AGA ATG TAT GGA TTA CCA CCC ACA GAA CCT ACC 2832
TAC TTT TGT CAA TGG GAT ATC AAT CTC GGA GAT TTA TGC ATT GAT TCA 2880
GAT ATT GAA TTT ATA AAG GGA TTC TTT AAT TCC TTT TAT AAG ATA GGT 2928
TTT GGC TAC AAT GAC TTG GAA AAT ATA TTA TTA TAT GAC ACT GAG ACC 2976
ATT AAT GAT ATG ACC TCG CTA ACC GTG CAC GTT GAA AAA ATA AGA ATA 3024
GGC CTT AAA GAT CCG GTG ATG AAA TCT CAA TCA GTT ATT AGT GCT GAA 3072
TCG ATA TTG TTT ACT TTG ATC GAC TTT GAA AAC GAA AAA TAT TCA CAA 3120
AGA ATA GAC GTG AAA ATT CCA AAA TTG ACA ATT TCG TTA AAT TGC GTG 3168
ATG GGC GAT GGC GTA GAC ACA TCA TTT CTC AAA TTC GAA ACA AAA TTA 3216
AGA TTT ACA AAC TTT GAG CAA TAC AAG GAT ATC GAT AAA AAA AGA TCA 3264
GAA CAA CGC AGA TAT ATA ACA ATA CAC GAT TCA CCC TAT CAT AGG TGT 3312
CCT TTT CTT CTT CCG CTG TTC TAT CAG GAT TCG GAT ACA TAC CAA AAC 3360
CTG TAC GGG GCT ATA GCA CCA TCT TCG TCT ATC CCA ACT TTA CCT CTT 3408
CCC ACT TTG CCT GAT ACT ATA GAT TAT ATC ATT GAA GAT ATT GTG GGC 3456
GAG TAT GCT ACC CTT CTG GAG ACC ACA AAT CCA TTC AAG AAC ATA TTC 3504
GCA GAA ACT CCA TCA ACT ATG GAG CCT TCA AGA GCC AGC TTC AGT GAA 3552
GAT GAT AAT GAC GAA GAA GCG GAC CCT TCA AGC TTC AAA CCT GTC GCT 3600
TTT ACA GAA GAC AGA AAC CAC GAA AGG GAT AAC TAT GTT GTT GAT GTT 3648
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GAT ATT GAA ATT GGG ATT GTG AAA CGA TTA AGC AAC CTT CAA GAA GGG 3792
ATC ACT TCT ATT TCA AAC ATT GAT ATC CAT ATT GCT TAT CTA AAT TTA 3840
ATC TGG CAA GAG ACA GGT GAG GAA GGT TTT GAG CTC TAT TTA GAT CGT 3888

ATT GAT TAT CAA ATG AGT GAA AAG TCT CTA GAG AAG AAC CGA ACA AAT 3936
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 AGG TTA CTT AAA TTG CAA GAT CTT ATT CCA CTC ATT GCA GCA GTG GGC 4848
 GAA GAT GAC AAA AGT GAT CCA AAA AAG GAG TTA TCA AAG CAA TTC AAA 4896
 ATG AAC ACC GTT TTA TTA GTG GAT AAA AGT GAA CTG CAA CTG GTC ATG 4944
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 CTA TGG GAA AAT CTA AAA GAT TCA ACT AGT CAA GCG GGT TCA TTG GTT 5040
 ATA TTT TCC CAG AAA TCG GAA GTG TGG TTA AAA CAC ACA TCT GTC ATT 5088
 TTG GGA GAA GCT CAA CTG CGC GAC TTT TCA GTT TTA GCG ACT ACT GAG 5136
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 CTT CAT TTT AGA GCA ATG AGT TCA ACT GAG CAA TTA GTA ACC GCT ATT 5232
 ACT GAA ATT AGG GAA AGT CTG ATG ATG ATT AAA GAG CGC ATA AAG TTT 5280
 AAA CCT AAA TCA AAG AAA AAG TCC CAA TTT GTC GAC CAG AAA ATT AAT 5328
 ACA GTC TTG TCA TGT TAT TTT TCA AAC GTT AGT TCT GAA GTT ATG CCG 5376
 CTC TCG CCA TTT TAT ATT CGT CAC GAA GCC AAG CAG CTT GAT ATA TAT 5424

TTT AAC AAA TTC GGT TCA AAT GAG ATT TTG TTA AGC ATA TGG GAT ACT 5472
 GAT TTT TTC ATG ACA TCG CAC CAG ACA AAG GAG CAA TAC CTA AGG TTT 5520
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 TCG TTG ATA AAC GTT GAC ATC TCA ATA TCT ATG ATT AAG TTA ACC TTT 5616
 TCG GAG CCG CGC CGT ATT GTA AAC AGT TTT TTA CAA GAT GAA AAG CTT 5664
 GCT TCT CAG GGT ATC AAT CTG TTA TAT TCC CTG AAG CCT TTA TTC TTT 5712
 AGT TCA AAT CTA CCA AAA AAA GAG AAG CAG GCA CCC TCG ATA ATG ATA 5760
 AAT TGG ACA TTA GAT ACT AGC ATT ACT TAT TTT GGT GTT CTT GTG CCA 5808
 GTG GCT TCC ACG TAT TTC GTG TTT GAA TTA CAT ATG CTG CTA CTT TCT 5856
 CTG ACC AAT ACG AAT AAC GGT ATG TTA CCA GAA GAA ACC AAG GTG ACG 5904
 GGA CAG TTT TCC ATC GAA AAC ATC CTA TTT CTA ATA AAG GAG CGG TCA 5952
 CTA CCC ATT GGT CTT TCC AAA TTA CTC GAC TTT TCC ATA AAA GTA TCA 6000
 ACC CTA CAA AGA ACG GTT GAT ACG GAG CAG TCA TTC CAA GTG GAA AGT 6048
 TCT CAT TTC AGG GTC TGC TTA TCT CCT GAT TCT CTA TTA AGA TTA ATG 6096
 TGG GGC GCG CAT AAA TTG CTA GAC TTG AGC CAT TAC TAT TCA AGA CGC 6144
 CAT GCC CCT AAT ATT TGG AAC ACT AAG ATG TTC ACC GGT AAA AGT GAT 6192
 AAG TCA AAA GAA ATG CCC ATA AAT TTC CGT TCA ATA CAC ATC CTG TCC 6240
 TAT AAA TTT TGT ATT GGG TGG ATA TTC CAG TAT GGA GCA GGC TCC AAT 6288
 CCT GGG TTA ATG TTA GGT TAT AAC AGA TTG TTT TCA GCA TAT GAA AAG 6336
 GAT TTT GGG AAA TTC ACA GTT GTG GAC GCT TTT TTC TCT GTT GCG AAT 6384
 GGT AAT ACC TCA AGC ACT TTT TTC TCT GAA GGA AAC GAG AAA GAC AAA 6432
 TAT AAT AGA AGT TTC TTG CCA AAC ATG CAA ATA TCC TAC TGG TTC AAA 6480
 AGA TGT GGT GAG TTG AAA GAT TGG TTT TTT AGA TTT CAT GGT GAA GCA 6528
 CTG GAT GTA AAC TTT GTC CCG TCA TTC ATG GAT GTC ATT GAG TCT ACT 6576
 TTA CAA TCC ATG CGA GCA TTT CAA GAG CTG AAA AAG AAC ATT CTG GAT 6624
 GTG TCC GAG AGT TTG CGT GCG GAA AAT GAT AAT TCT TAT GCT AGT ACC 6672
 AGT GTC GAA AGT GCT TCG AGT AGT TTG GCT CCC TTT CTC GAT AAC ATT 6720
 AGA TCT GTT AAC TCA AAT TTC AAG TAT GAC GGT GGT GTA TTT AGG GTT 6768
 TAC ACG TAC GAA GAT ATT GAA ACC AAG AGT GAG CCA TCT TTT GAA ATA 6816
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 AAA GTT AAG CCA CAT AAA TTC AGA ACA TTA ATC ACT GTC GAC CCA ACG 6912
 CAT AAT ACT TTG TAT GCG GGA TGT GCT CCT TTA TTA ATG GAA TTT TCT 6960

GAA AGT CTG CAA AAG ATG ATA AAG AAA CAT AGC ACC GAC GAA AAA CCA 7008
AAC TTT ACA AAA CCT TCT TCA CAG AAT GTT GAT TAT AAG CGA CTT TTG 7056
GAT CAA TTT GAT GTG GCT GTA AAA CTA ACA TCA GCC AAG CAA CAG CTA 7104
AGT TTG AGC TGT GAA CCA AAA GCT AAG GTT CAG GCA GAT GTT GGA TTT 7152
GAA TCG TTT TTG TTC AGT ATG GCT ACC AAT GAG TTC GAC TCT GAA CAG 7200
CCT TTG GAG TTT TCT TTA ACT CTA GAA CAC ACA AAA GCG TCC ATT AAG 7248
CAC ATA TTT TCA AGA GAA GTA AGT ACG TCC TTT GAA GTT GGT TTC ATG 7296
GAC TTG ACG CTT TTA TTT ACA CAT CCT GAT GTA ATC AGT ATG TAT GGA 7344
ACG GGG TTG GTT TCT GAT CTA AGC GTC TTC TTC AAT GTA AAG CAG CTC 7392
CAG AAC CTG TAT TTA TTC TTG GAC ATA TGG AGG TTC AGT AGC ATT TTA 7440
CAC ACA CGG CCA GTG CAA AGA ACT GTT AAT AAG GAA ATT GAA ATG AGT 7488
TCA TTA ACA TCA ACC AAC TAT GCC GAT GCA GGT ACG GAA ATA CCC TGG 7536
TGC TTT ACA TTA ATT TTT ACA AAT GTT AGC GGA GAC GTT GAT TTG GGT 7584
CCT TCT CTC GGT ATG ATT TCA TTA AGG ACA CAA AGA ACA TGG CTG GCC 7632
ACA GAT CAT TAT AAC GAG AAG CGG CAG TTA CTG CAT GCT TTC ACT GAC 7680
GGT ATT AGC TTG ACA TCA GAA GGT AGA CTG AGT GGT TTA TTT GAA GTT 7728
GCG AAT GCA AGT TGG TTA TCA GAA GTA AAA TGG CCA CCT GAA AAA AGC 7776
AAA AAT ACT CAT CCA TTA GTT TCC ACC TCC CTG AAT ATT GAT GAT ATA 7824
GCG GTA AAG GCT GCT TTT GAT TAT CAT ATG TTC TTA ATC GGC ACT ATA 7872
AGT AAC ATA CAC TTC CAT CTT CAT AAT GAA AAG GAT GCC AAG GGG GTT 7920
CTA CCT GAT TTG CTG CAG GTC TCT TTT TCA TCA GAT GAA ATT ATC CTC 7968
AGC TCT ACT GCA TTA GTT GTA GCA AAT ATA CTG GAT ATC TAC AAC ACC 8016
ATT GTA CGT ATG AGG CAG GAT AAT AAA ATA TCG TAT ATG GAG ACG TTG 8064
AGA GAT TCC AAT CCT GGT GAA TCT AGG CAA CCA ATA TTA TAC AAA GAC 8112
ATT TTA AGA TCG CTG AAA TTA CTC AGA ACT GAT CTC TCG GTG AAT ATC 8160
TCC TCT TCA AAG GTC CAG ATT TCG CCA ATA TCT TTA TTC GAT GTG GAA 8208
GTG TTA GTA ATA AGA ATT GAC AAA GTC TCT ATA CGT TCC GAA ACA CAT 8256
TCG GGG AAA AAA TTA AAG ACA GAT TTG CAA CTA CAA GTT TTA GAT GTT 8304
TCT GCA GCG CTT TCT ACT TCC AAA GAA GAA TTA GAT GAG GAA GTT GGA 8352
GCT TCC ATT GCT ATT GAT GAT TAC ATG CAT TAT GCT TCC AAG ATT GTC 8400
GGT GGT ACT ATC ATT GAT ATT CCA AAA CTT GCT GTT CAT ATG ACA ACT 8448
TTA CAA GAA GAA AAG ACA AAT AAT TTA GAA TAT CTA TTT GCT TGC TCT 8496

TTT TCA GAC AAA ATA TCT GTA AGG TGG AAT CTA GGG CCT GTA GAC TTC 8544
 ATA AAG GAA ATG TGG ACT ACA CAT GTC AAA GCA CTG GCA GTT CGT CGA 8592
 TCC CAG GTA GCA AAT ATT TCC TTT GGA CAA ACT GAG GAA GAA CTT GAA 8640
 GAA TCA ATT AAA AAG GAA GAA GCC GCT TCA AAG TTT AAT TAT ATT GCA 8688
 CTA GAA GAA CCG CAG ATC GAA GTG CCT CAG ATA AGA GAT CTG GGA GAC 8736
 GCC ACT CCA CCT ATG GAA TGG TTT GGT GTC AAT AGA AAA AAA TTT CCG 8784
 AAA TTC ACT CAC CAA ACC GCA GTT ATC CCC GTC CAA AAG CTT GTT TAT 8832
 CTT GCA GAA AAG CAG TAT GTC AAG ATA CTA GAT GAT ACG CAT 8874

(2) INFORMATION FOR SEQ ID NO: 2 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2958 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(B) STRAIN: X2180-1B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

Met Glu Ala Ile Ser Gln Leu Arg Gly Val Pro Leu Thr His Gln Lys
 1 5 10 15
 Asp Phe Ser Trp Val Phe Leu Val Asp Trp Ile Leu Thr Val Val Val
 20 25 30
 Cys Leu Thr Met Ile Phe Tyr Met Gly Arg Ile Tyr Ala Tyr Leu Val
 35 40 45
 Ser Phe Ile Leu Glu Trp Leu Leu Trp Lys Arg Ala Lys Ile Lys Ile
 50 55 60
 Asn Val Glu Thr Leu Arg Val Ser Leu Leu Gly Gly Arg Ile His Phe
 65 70 75 80
 Lys Asn Leu Ser Val Ile His Lys Asp Tyr Thr Ile Ser Val Leu Glu
 85 90 95
 Gly Ser Leu Thr Trp Lys Tyr Trp Leu Leu Asn Cys Arg Lys Ala Glu
 100 105 110
 Leu Ile Glu Asn Asn Lys Ser Ser Ser Gly Lys Lys Ala Lys Leu Pro
 115 120 125

Cys Lys Ile Ser Val Glu Cys Glu Gly Leu Glu Ile Phe Ile Tyr Asn
 130 135 140
 Arg Thr Val Ala Tyr Asp Asn Val Ile Asn Leu Leu Ser Lys Asp Glu
 145 150 155 160
 Arg Asp Lys Phe Glu Lys Tyr Leu Asn Glu His Ser Phe Pro Glu Pro
 165 170 175
 Phe Ser Asp Gly Ser Ser Ala Asp Lys Leu Asp Glu Asp Leu Ser Glu
 180 185 190
 Ser Ala Tyr Thr Thr Asn Ser Asp Ala Ser Ile Val Asn Asp Arg Asp
 195 200 205
 Tyr Gln Glu Thr Asp Ile Gly Lys His Pro Lys Leu Leu Met Phe Leu
 210 215 220
 Pro Ile Glu Leu Lys Phe Ser Arg Gly Ser Leu Leu Leu Gly Asn Lys
 225 230 235 240
 Phe Thr Pro Ser Val Met Ile Leu Ser Tyr Glu Ser Gly Lys Gly Ile
 245 250 255
 Ile Asp Val Leu Pro Pro Lys Glu Arg Leu Asp Leu Tyr Arg Asn Lys
 260 265 270
 Thr Gln Met Glu Phe Lys Asn Phe Glu Ile Ser Ile Lys Gln Asn Ile
 275 280 285
 Gly Tyr Asp Asp Ala Ile Gly Leu Lys Phe Lys Ile Asp Arg Gly Lys
 290 295 300
 Val Ser Lys Leu Trp Lys Thr Phe Val Arg Val Phe Gln Ile Val Thr
 305 310 315 320
 Lys Pro Val Val Pro Lys Lys Thr Lys Lys Ser Ala Gly Thr Ser Asp
 325 330 335
 Asp Asn Phe Tyr His Lys Trp Lys Gly Leu Ser Leu Tyr Lys Ala Ser
 340 345 350
 Ala Gly Asp Ala Lys Ala Ser Asp Leu Asp Asp Val Glu Phe Asp Leu
 355 360 365
 Thr Asn His Glu Tyr Ala Lys Phe Thr Ser Ile Leu Lys Cys Pro Lys
 370 375 380

Val Thr Ile Ala Tyr Asp Val Asp Val Pro Gly Val Val Pro His Gly			
385	390	395	400
Ala His Pro Thr Ile Pro Asp Ile Asp Gly Pro Asp Val Gly Asn Asn			
	405	410	415
Gly Ala Pro Pro Asp Phe Ala Leu Asp Val Gln Ile His Gly Gly Ser			
	420	425	430
Ile Cys Tyr Gly Pro Trp Ala Gln Arg Gln Val Ser His Leu Gln Arg			
	435	440	445
Val Leu Ser Pro Val Val Ser Arg Thr Ala Lys Pro Ile Lys Lys Leu			
	450	455	460
Pro Pro Gly Ser Arg Arg Ile Tyr Thr Leu Phe Arg Met Asn Ile Ser			
465	470	475	480
Ile Met Glu Asp Thr Thr Trp Arg Ile Pro Thr Arg Glu Ser Ser Lys			
	485	490	495
Asp Pro Glu Phe Leu Lys His Tyr Lys Glu Thr Asn Glu Glu Tyr Arg			
	500	505	510
Pro Phe Gly Trp Met Asp Leu Arg Phe Cys Lys Asp Thr Tyr Ala Asn			
	515	520	525
Phe Asn Ile Ser Val Cys Pro Thr Val Gln Gly Phe Gln Asn Asn Phe			
	530	535	540
His Val His Phe Leu Glu Thr Glu Ile Arg Ser Ser Val Asn His Asp			
545	550	555	560
Ile Leu Leu Lys Ser Lys Val Phe Asp Ile Asp Gly Asp Ile Gly Tyr			
	565	570	575
Pro Leu Gly Trp Asn Ser Lys Ala Ile Trp Ile Ile Asn Met Lys Ser			
	580	585	590
Glu Gln Leu Glu Ala Phe Leu Leu Arg Glu His Ile Thr Leu Val Ala			
	595	600	605
Asp Thr Leu Ser Asp Phe Ser Ala Gly Asp Pro Thr Pro Tyr Glu Leu			
	610	615	620
Phe Arg Pro Phe Val Tyr Lys Val Asn Trp Glu Met Glu Gly Tyr Ser			
625	630	635	640

Ile Tyr Leu Asn Val Asn Asp His Asn Ile Val Asn Asn Pro Leu Asp			
645	650	655	
Phe Asn Glu Asn Cys Tyr Leu Ser Leu His Gly Asp Lys Leu Ser Ile			
660	665	670	
Asp Val Thr Val Pro Arg Glu Ser Ile Leu Gly Thr Tyr Thr Asp Met			
675	680	685	
Ser Tyr Glu Ile Ser Thr Pro Met Phe Arg Met Met Leu Asn Thr Pro			
690	695	700	
Pro Trp Asn Thr Leu Asn Glu Phe Met Lys His Lys Glu Val Gly Arg			
705	710	715	720
Ala Tyr Asp Phe Thr Ile Lys Gly Ser Tyr Leu Leu Tyr Ser Glu Leu			
725	730	735	
Asp Ile Asp Asn Val Asp Thr Leu Val Ile Glu Cys Asn Ser Lys Ser			
740	745	750	
Thr Val Leu His Cys Tyr Gly Phe Val Met Arg Tyr Leu Thr Asn Val			
755	760	765	
Lys Met Asn Tyr Phe Gly Glu Phe Phe Asn Phe Val Thr Ser Glu Glu			
770	775	780	
Tyr Thr Gly Val Leu Gly Ala Arg Glu Val Gly Asp Val Thr Thr Lys			
785	790	795	800
Ser Ser Val Ala Asp Leu Ala Ser Thr Val Asp Ser Gly Tyr Gln Asn			
805	810	815	
Ser Ser Leu Lys Asn Glu Ser Glu Asp Lys Gly Pro Met Lys Arg Ser			
820	825	830	
Asp Leu Lys Arg Thr Thr Asn Glu Thr Asp Ile Trp Phe Thr Phe Ser			
835	840	845	
Val Trp Asp Gly Ala Leu Ile Leu Pro Glu Thr Ile Tyr Ser Phe Asp			
850	855	860	
Pro Cys Ile Ala Leu His Phe Ala Glu Leu Val Val Asp Phe Arg Ser			
865	870	875	880
Cys Asn Tyr Tyr Met Asp Ile Met Ala Val Leu Asn Gly Thr Ser Ile			
885	890	895	

Lys Arg His Val Ser Lys Gln Ile Asn Glu Val Phe Asp Phe Ile Arg
 900 905 910
 Arg Asn Asn Gly Ala Asp Glu Gln Glu His Gly Leu Leu Ser Asp Leu
 915 920 925
 Thr Ile His Gly His Arg Met Tyr Gly Leu Pro Pro Thr Glu Pro Thr
 930 935 940
 Tyr Phe Cys Gln Trp Asp Ile Asn Leu Gly Asp Leu Cys Ile Asp Ser
 945 950 955 960
 Asp Ile Glu Phe Ile Lys Gly Phe Phe Asn Ser Phe Tyr Lys Ile Gly
 965 970 975
 Phe Gly Tyr Asn Asp Leu Glu Asn Ile Leu Leu Tyr Asp Thr Glu Thr
 980 985 990
 Ile Asn Asp Met Thr Ser Leu Thr Val His Val Glu Lys Ile Arg Ile
 995 1000 1005
 Gly Leu Lys Asp Pro Val Met Lys Ser Gln Ser Val Ile Ser Ala Glu
 1010 1015 1020
 Ser Ile Leu Phe Thr Leu Ile Asp Phe Glu Asn Glu Lys Tyr Ser Gln
 1025 1030 1035
 1040 Arg Ile Asp Val Lys Ile Pro Lys Leu Thr Ile Ser Leu Asn Cys Val
 1045 1050 1055
 Met Gly Asp Gly Val Asp Thr Ser Phe Leu Lys Phe Glu Thr Lys Leu
 1060 1065 1070
 Arg Phe Thr Asn Phe Glu Gln Tyr Lys Asp Ile Asp Lys Lys Arg Ser
 1075 1080 1085
 Glu Gln Arg Arg Tyr Ile Thr Ile His Asp Ser Pro Tyr His Arg Cys
 1090 1095 1100
 Pro Phe Leu Leu Pro Leu Phe Tyr Gln Asp Ser Asp Thr Tyr Gln Asn
 1105 1110 1115 1120
 Leu Tyr Gly Ala Ile Ala Pro Ser Ser Ser Ile Pro Thr Leu Pro Leu
 1125 1130 1135
 Pro Thr Leu Pro Asp Thr Ile Asp Tyr Ile Ile Glu Asp Ile Val Gly
 1140 1145 1150

Glu Tyr Ala Thr Leu Leu Glu Thr Thr Asn Pro Phe Lys Asn Ile Phe			
1155	1160	1165	
Ala Glu Thr Pro Ser Thr Met Glu Pro Ser Arg Ala Ser Phe Ser Glu			
1170	1175	1180	
Asp Asp Asn Asp Glu Glu Ala Asp Pro Ser Ser Phe Lys Pro Val Ala			
1185	1190	1195	1200
Phe Thr Glu Asp Arg Asn His Glu Arg Asp Asn Tyr Val Val Asp Val			
1205	1210	1215	
Ser Tyr Ile Leu Leu Asp Val Asp Pro Leu Leu Phe Ile Phe Ala Lys			
1220	1225	1230	
Ser Leu Leu Glu Gln Leu Tyr Ser Glu Asn Met Val Gln Val Leu Asp			
1235	1240	1245	
Asp Ile Glu Ile Gly Ile Val Lys Arg Leu Ser Asn Leu Gln Glu Gly			
1250	1255	1260	
Ile Thr Ser Ile Ser Asn Ile Asp Ile His Ile Ala Tyr Leu Asn Leu			
1265	1270	1275	1280
Ile Trp Gln Glu Thr Gly Glu Glu Gly Phe Glu Leu Tyr Leu Asp Arg			
1285	1290	1295	
Ile Asp Tyr Gln Met Ser Glu Lys Ser Leu Glu Lys Asn Arg Thr Asn			
1300	1305	1310	
Lys Leu Leu Glu Val Ala Ala Leu Ala Lys Val Lys Thr Val Arg Val			
1315	1320	1325	
Thr Val Asn Gln Lys Lys Asn Pro Asp Leu Ser Glu Asp Arg Pro Pro			
1330	1335	1340	
Ala Leu Ser Leu Gly Ile Glu Gly Phe Glu Val Trp Ser Ser Thr Glu			
1345	1350	1355	1360
Asp Arg Gln Val Asn Ser Leu Asn Leu Thr Ser Ser Asp Ile Thr Ile			
1365	1370	1375	
Asp Glu Ser Gln Met Glu Trp Leu Phe Glu Tyr Cys Ser Asp Gln Gly			
1380	1385	1390	
Asn Leu Ile Gln Glu Val Cys Thr Ser Phe Asn Ser Ile Gln Asn Thr			
1395	1400	1405	

Arg Ser Asn Ser Lys Thr Glu Leu Ile Ser Lys Leu Thr Ala Ala Ser			
1410	1415	1420	
Glu Tyr Tyr Gln Ile Ser His Asp Pro Tyr Val Ile Thr Lys Pro Ala			
1425	1430	1435	1440
Phe Ile Met Arg Leu Ser Lys Gly His Val Arg Glu Asn Arg Ser Trp			
	1445	1450	1455
Lys Ile Ile Thr Arg Leu Arg His Ile Leu Thr Tyr Leu Pro Asp Asp			
	1460	1465	1470
Trp Gln Ser Asn Ile Asp Glu Val Leu Lys Glu Lys Lys Tyr Thr Ser			
	1475	1480	1485
Ala Lys Asp Ala Lys Asn Ile Phe Met Ser Val Phe Ser Thr Trp Arg			
	1490	1495	1500
Asn Trp Glu Phe Ser Asp Val Ala Arg Ser Tyr Ile Tyr Gly Lys Leu			
1505	1510	1515	1520
Phe Thr Ala Glu Asn Glu Lys His Lys Gln Asn Leu Ile Lys Lys Leu			
	1525	1530	1535
Leu Lys Cys Thr Met Gly Ser Phe Tyr Leu Thr Val Tyr Gly Glu Gly			
	1540	1545	1550
Tyr Glu Val Glu His Asn Phe Val Val Ala Asp Ala Asn Leu Val Val			
	1555	1560	1565
Asp Leu Thr Pro Pro Val Thr Ser Leu Pro Ser Asn Arg Glu Glu Thr			
	1570	1575	1580
Ile Glu Ile Thr Gly Arg Val Gly Ser Val Lys Gly Lys Phe Ser Asp			
1585	1590	1595	1600
Arg Leu Leu Lys Leu Gln Asp Leu Ile Pro Leu Ile Ala Ala Val Gly			
	1605	1610	1615
Glu Asp Asp Lys Ser Asp Pro Lys Lys Glu Leu Ser Lys Gln Phe Lys			
	1620	1625	1630
Met Asn Thr Val Leu Leu Val Asp Lys Ser Glu Leu Gln Leu Val Met			
	1635	1640	1645
Asp Gln Thr Lys Leu Met Ser Arg Thr Val Gly Gly Arg Val Ser Leu			
1650	1655	1660	

Leu Trp Glu Asn Leu Lys Asp Ser Thr Ser Gln Ala Gly Ser Leu Val
 1665 1670 1675 1680
 Ile Phe Ser Gln Lys Ser Glu Val Trp Leu Lys His Thr Ser Val Ile
 1685 1690 1695
 Leu Gly Glu Ala Gln Leu Arg Asp Phe Ser Val Leu Ala Thr Thr Glu
 1700 1705 1710
 Ala Trp Ser His Lys Pro Thr Ile Leu Ile Asn Asn Gln Cys Ala Asp
 1715 1720 1725
 Leu His Phe Arg Ala Met Ser Ser Thr Glu Gln Leu Val Thr Ala Ile
 1730 1735 1740
 Thr Glu Ile Arg Glu Ser Leu Met Met Ile Lys Glu Arg Ile Lys Phe
 1745 1750 1755 1760
 Lys Pro Lys Ser Lys Lys Lys Ser Gln Phe Val Asp Gln Lys Ile Asn
 1765 1770 1775
 Thr Val Leu Ser Cys Tyr Phe Ser Asn Val Ser Ser Glu Val Met Pro
 1780 1785 1790
 Leu Ser Pro Phe Tyr Ile Arg His Glu Ala Lys Gln Leu Asp Ile Tyr
 1795 1800 1805
 Phe Asn Lys Phe Gly Ser Asn Glu Ile Leu Leu Ser Ile Trp Asp Thr
 1810 1815 1820
 Asp Phe Phe Met Thr Ser His Gln Thr Lys Glu Gln Tyr Leu Arg Phe
 1825 1830 1835 1840
 Ser Phe Gly Asp Ile Glu Ile Lys Gly Gly Ile Ser Arg Glu Gly Tyr
 1845 1850 1855
 Ser Leu Ile Asn Val Asp Ile Ser Ile Ser Met Ile Lys Leu Thr Phe
 1860 1865 1870
 Ser Glu Pro Arg Arg Ile Val Asn Ser Phe Leu Gln Asp Glu Lys Leu
 1875 1880 1885
 Ala Ser Gln Gly Ile Asn Leu Leu Tyr Ser Leu Lys Pro Leu Phe Phe
 1890 1895 1900
 Ser Ser Asn Leu Pro Lys Lys Glu Lys Gln Ala Pro Ser Ile Met Ile
 1905 1910 1915 1920

Asn Trp Thr Leu Asp Thr Ser Ile Thr Tyr Phe Gly Val Leu Val Pro			
	1925	1930	1935
Val Ala Ser Thr Tyr Phe Val Phe Glu Leu His Met Leu Leu Leu Ser	1940	1945	1950
Leu Thr Asn Thr Asn Asn Gly Met Leu Pro Glu Glu Thr Lys Val Thr			
	1955	1960	1965
Gly Gln Phe Ser Ile Glu Asn Ile Leu Phe Leu Ile Lys Glu Arg Ser			
	1970	1975	1980
Leu Pro Ile Gly Leu Ser Lys Leu Leu Asp Phe Ser Ile Lys Val Ser			
	1985	1990	1995
Thr Leu Gln Arg Thr Val Asp Thr Glu Gln Ser Phe Gln Val Glu Ser			
	2005	2010	2015
Ser His Phe Arg Val Cys Leu Ser Pro Asp Ser Leu Leu Arg Leu Met			
	2020	2025	2030
Trp Gly Ala His Lys Leu Leu Asp Leu Ser His Tyr Tyr Ser Arg Arg			
	2035	2040	2045
His Ala Pro Asn Ile Trp Asn Thr Lys Met Phe Thr Gly Lys Ser Asp			
	2050	2055	2060
Lys Ser Lys Glu Met Pro Ile Asn Phe Arg Ser Ile His Ile Leu Ser			
	2065	2070	2075
Tyr Lys Phe Cys Ile Gly Trp Ile Phe Gln Tyr Gly Ala Gly Ser Asn			
	2085	2090	2095
Pro Gly Leu Met Leu Gly Tyr Asn Arg Leu Phe Ser Ala Tyr Glu Lys			
	2100	2105	2110
Asp Phe Gly Lys Phe Thr Val Val Asp Ala Phe Phe Ser Val Ala Asn			
	2115	2120	2125
Gly Asn Thr Ser Ser Thr Phe Phe Ser Glu Gly Asn Glu Lys Asp Lys			
	2130	2135	2140
Tyr Asn Arg Ser Phe Leu Pro Asn Met Gln Ile Ser Tyr Trp Phe Lys			
	2145	2150	2155
Arg Cys Gly Glu Leu Lys Asp Trp Phe Phe Arg Phe His Gly Glu Ala			
	2165	2170	2175
Leu Asp Val Asn Phe Val Pro Ser Phe Met Asp Val Ile Glu Ser Thr			

2180	2185	2190
Leu Gln Ser Met Arg Ala Phe Gln Glu Leu Lys Lys Asn Ile Leu Asp		
2195	2200	2205
Val Ser Glu Ser Leu Arg Ala Glu Asn Asp Asn Ser Tyr Ala Ser Thr		
2210	2215	2220
Ser Val Glu Ser Ala Ser Ser Ser Leu Ala Pro Phe Leu Asp Asn Ile		
2225	2230	2235
Arg Ser Val Asn Ser Asn Phe Lys Tyr Asp Gly Gly Val Phe Arg Val		
2245	2250	2255
Tyr Thr Tyr Glu Asp Ile Glu Thr Lys Ser Glu Pro Ser Phe Glu Ile		
2260	2265	2270
Lys Ser Pro Val Val Thr Ile Asn Cys Thr Tyr Lys His Asp Glu Asp		
2275	2280	2285
Lys Val Lys Pro His Lys Phe Arg Thr Leu Ile Thr Val Asp Pro Thr		
2290	2295	2300
His Asn Thr Leu Tyr Ala Gly Cys Ala Pro Leu Leu Met Glu Phe Ser		
2305	2310	2315
Glu Ser Leu Gln Lys Met Ile Lys Lys His Ser Thr Asp Glu Lys Pro		
2325	2330	2335
Asn Phe Thr Lys Pro Ser Ser Gln Asn Val Asp Tyr Lys Arg Leu Leu		
2340	2345	2350
Asp Gln Phe Asp Val Ala Val Lys Leu Thr Ser Ala Lys Gln Gln Leu		
2355	2360	2365
Ser Leu Ser Cys Glu Pro Lys Ala Lys Val Gln Ala Asp Val Gly Phe		
2370	2375	2380
Glu Ser Phe Leu Phe Ser Met Ala Thr Asn Glu Phe Asp Ser Glu Gln		
2385	2390	2395
Pro Leu Glu Phe Ser Leu Thr Leu Glu His Thr Lys Ala Ser Ile Lys		
2405	2410	2415
His Ile Phe Ser Arg Glu Val Ser Thr Ser Phe Glu Val Gly Phe Met		
2420	2425	2430
Asp Leu Thr Leu Leu Phe Thr His Pro Asp Val Ile Ser Met Tyr Gly		

2435	2440	2445	
Thr Gly Leu Val Ser Asp Leu Ser Val Phe Phe Asn Val Lys Gln Leu			
2450	2455	2460	
Gln Asn Leu Tyr Leu Phe Leu Asp Ile Trp Arg Phe Ser Ser Ile Leu			
2465	2470	2475	2480
His Thr Arg Pro Val Gln Arg Thr Val Asn Lys Glu Ile Glu Met Ser			
2485	2490	2495	
Ser Leu Thr Ser Thr Asn Tyr Ala Asp Ala Gly Thr Glu Ile Pro Trp			
2500	2505	2510	
Cys Phe Thr Leu Ile Phe Thr Asn Val Ser Gly Asp Val Asp Leu Gly			
2515	2520	2525	
Pro Ser Leu Gly Met Ile Ser Leu Arg Thr Gln Arg Thr Trp Leu Ala			
2530	2535	2540	
Thr Asp His Tyr Asn Glu Lys Arg Gln Leu Leu His Ala Phe Thr Asp			
2545	2550	2555	2560
Gly Ile Ser Leu Thr Ser Glu Gly Arg Leu Ser Gly Leu Phe Glu Val			
2565	2570	2575	
Ala Asn Ala Ser Trp Leu Ser Glu Val Lys Trp Pro Pro Glu Lys Ser			
2580	2585	2590	
Lys Asn Thr His Pro Leu Val Ser Thr Ser Leu Asn Ile Asp Asp Ile			
2595	2600	2605	
Ala Val Lys Ala Ala Phe Asp Tyr His Met Phe Leu Ile Gly Thr Ile			
2610	2615	2620	
Ser Asn Ile His Phe His Leu His Asn Glu Lys Asp Ala Lys Gly Val			
2625	2630	2635	2640
Leu Pro Asp Leu Leu Gln Val Ser Phe Ser Ser Asp Glu Ile Ile Leu			
2645	2650	2655	
Ser Ser Thr Ala Leu Val Val Ala Asn Ile Leu Asp Ile Tyr Asn Thr			
2660	2665	2670	
Ile Val Arg Met Arg Gln Asp Asn Lys Ile Ser Tyr Met Glu Thr Leu			
2675	2680	2685	
Arg Asp Ser Asn Pro Gly Glu Ser Arg Gln Pro Ile Leu Tyr Lys Asp			

2690	2695	2700	
Ile Leu Arg Ser Leu Lys Leu Leu Arg Thr Asp Leu Ser Val Asn Ile			
2705	2710	2715	2720
Ser Ser Ser Lys Val Gln Ile Ser Pro Ile Ser Leu Phe Asp Val Glu			
	2725	2730	2735
Val Leu Val Ile Arg Ile Asp Lys Val Ser Ile Arg Ser Glu Thr His			
	2740	2745	2750
Ser Gly Lys Lys Leu Lys Thr Asp Leu Gln Leu Gln Val Leu Asp Val			
	2755	2760	2765
Ser Ala Ala Leu Ser Thr Ser Lys Glu Glu Leu Asp Glu Glu Val Gly			
	2770	2775	2780
Ala Ser Ile Ala Ile Asp Asp Tyr Met His Tyr Ala Ser Lys Ile Val			
2785	2790	2795	2800
Gly Gly Thr Ile Ile Asp Ile Pro Lys Leu Ala Val His Met Thr Thr			
	2805	2810	2815
Leu Gln Glu Glu Lys Thr Asn Asn Leu Glu Tyr Leu Phe Ala Cys Ser			
	2820	2825	2830
Phe Ser Asp Lys Ile Ser Val Arg Trp Asn Leu Gly Pro Val Asp Phe			
	2835	2840	2845
Ile Lys Glu Met Trp Thr Thr His Val Lys Ala Leu Ala Val Arg Arg			
	2850	2855	2860
Ser Gln Val Ala Asn Ile Ser Phe Gly Gln Thr Glu Glu Glu Leu Glu			
2865	2870	2875	2880
Glu Ser Ile Lys Lys Glu Glu Ala Ala Ser Lys Phe Asn Tyr Ile Ala			
	2885	2890	2895
Leu Glu Glu Pro Gln Ile Glu Val Pro Gln Ile Arg Asp Leu Gly Asp			
	2900	2905	2910
Ala Thr Pro Pro Met Glu Trp Phe Gly Val Asn Arg Lys Lys Phe Pro			
	2915	2920	2925
Lys Phe Thr His Gln Thr Ala Val Ile Pro Val Gln Lys Leu Val Tyr			
	2930	2935	2940
Leu Ala Glu Lys Gln Tyr Val Lys Ile Leu Asp Asp Thr His			

2945

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